

blast result

Exhibit I

lambda K H
0.329 0.145 0.465

Gapped
Lambda K H
0.270 0.0470 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 5098040
Number of Sequences: 113759
Number of extensions: 179204
Number of successful extensions: 883
Number of sequences better than 10.0: 473
Number of HSP's better than 10.0 without gapping: 469
Number of HSP's successfully gapped in prelim test: 4
Number of HSP's that attempted gapping in prelim test: 361
Number of HSP's gapped (non-prelim): 522
length of query: 99
length of database: 24,820,038
effective HSP length: 40
effective length of query: 59
effective length of database: 20269678
effective search space: 1195911002
effective search space used: 1195911002
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 40 (21.8 bits)
S2: 58 (27.0 bits)
BLASTP 2.0.9 [May-07-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 51-15-4-A12-CL11_3C
(121 letters)

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
113,759 sequences; 24,820,038 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
GSP:Y35930 Y35930 Extended human secreted protein sequence, SEQ...	263	6e-71
GSP:Y91513 Y91513 Human secreted protein sequence encoded by ge...	263	6e-71
GSP:Y12687 Y12687 Human 5' EST secreted protein SEQ ID NO:277.	245	2e-65
SP:P04118 COL_HUMAN COLIPASE PRECURSOR. >PIR:A42568 A33949 A031...	55	3e-08
PIR:S37649 S37649 high-sulfur keratin - human >STR:Q07628 Q0762...	32	0.28
GSP:Y44934 Y44934 Human dickkopf-1 homolog 3 protein.	32	0.36
STR:Q9UIU3 Q9UIU3 DICKKOPF-2 PROTEIN (FRAGMENT). >GNP:AB035181 ...	31	0.82
GSP:W73019 W73019 Human cysteine-rich secreted protein CRSP-4.	31	0.82
GSP:Y99360 Y99360 Human PRO1316 (UNQ682) amino acid sequence SE...	31	0.82
GSP:Y92074 Y92074 Human DKR-2 splice variant, DKR-2a.	31	0.82
STR:Q9Y6P9 Q9Y6P9 HJAG2.DEL-E6. >GNP:AF029779 AF029779_1 Homo s...	30	1.8
STR:Q9Y219 Q9Y219 JAGGED 2. >GNP:AF020201 AF020201_1 Homo sapie...	30	1.8
STR:Q9UNK8 Q9UNK8 JAGGED2. >GNP:AF111170 AF111170_2 Homo sapien...	30	1.8
STR:Q9Y6Q0 Q9Y6Q0 JAGGED2. >GNP:AF029778 AF029778_1 Homo sapien...	30	1.8
STR:Q9UE99 Q9UE99 JAGGED 2. >GNP:AF003521 AF003521_1 Homo sapie...	30	1.8
GSP:W05834 W05834 Human Serrate-2 (HJ2). >GSP:Y59598 Y59598 Hum...	30	1.8
GSP:W44298 W44298 Human serrate 2 protein fragment.	30	1.8
GSP:W44299 W44299 Human serrate 2.	30	1.8
GSP:W87895 W87895 Human JAGGED2 protein.	30	1.8
STR:Q9UQ12 Q9UQ12 KIAA0868 PROTEIN (FRAGMENT). >GNP:AB020675 AB...	29	2.4
STR:Q9UHC6 Q9UHC6 CELL RECOGNITION MOLECULE CASPR2. >GNP:AF1936...	29	2.4
STR:Q9UE17 Q9UE17 JAGGED2 PROTEIN (FRAGMENT). >GNP:Y14330 Y1433...	29	4.1
GSP:Y04262 Y04262 Human vascular smooth muscle cell growth f...		

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79 QYRACPLRLNLTCIYSKNEKW--LSIAYGRCQKIGRQKLAKKM 119
 + P + C+ S +W S+ G+ + RQ++ K +
 ct: 603 EKCMMPECHTIPCLLSPWSEWSDCSVTGKGMRT-RQRMLKSL 644

>STR:094862|094862|KIAA0762 PROTEIN (FRAGMENT).

>GNP:AB018305|AB018305_1|Homo sapiens mRNA for KIAA0762
 protein, partial cds.
 Length = 624

Score = 28.2 bits (61), Expect = 5.4
 Identities = 21/103 (20%), Positives = 39/103 (37%), Gaps = 18/103 (17%)

Query: 34 ELKESCIRNQDCETGCCQRAP----DNCESHCAE-----KGSEGLCQTQVFFG 78
 E E C N++C C D C + C ++GS+C+ +
 Sbjct: 360 EETEKCTVNEECSPSSCLMTEWGEWDECSATCGMGKKRHRMIKMPADGSMCKAETSQA 419

Query: 79 QYRACPLRLNLTCIYSKNEKW--LSIAYGRCQKIGRQKLAKKM 119
 + P + C+ S +W S+ G+ + RQ++ K +
 Sbjct: 420 EKCMMPECHTIPCLLSPWSEWSDCSVTGKGMRT-RQRMLKSL 461

>GSP:W73018|W73018|Human cysteine-rich secreted protein CRSP-3.

>GSP:Y41757|Y41757|Human PRO1008 protein sequence.
 >GSP:Y92071|Y92071|Human DKR-1.
 >STR:094907|094907|DICKKOPF-1 (HDKK-1) PROTEIN (HDKK-1).
 >GNP:AB020315|AB020315_1|Homo sapiens Dickkopf-1
 (hdkk-1) gene, 3rd, 4th coding region and complete cds;
 homologue of mouse dkk-1 gene:Acc# AF030433.
 >GNP:AF127563|AF127563_1|Homo sapiens Sk/Dkk-1 protein
 precursor, mRNA, complete cds; secreted wnt inhibitor
 with affinity for heparin sepharose.
 >GNP:AF177394|AF177394_1|Homo sapiens dickkopf-1 (DKK-1)
 mRNA, complete cds; secreted protein.
 >GNP:AF261158|AF261158_1|Homo sapiens dickkopf homolog 1
 (DKK1) gene, exons 3 and 4, and complete cds.
 Length = 266

Score = 27.8 bits (60), Expect = 7.1
 Identities = 23/86 (26%), Positives = 34/86 (38%), Gaps = 17/86 (19%)

Query: 22 RGSLSPTKYNNLELKEK-CIRNQDCETGCCQRAPDNCESH-----CAEKGSEGLCQTQV 75
 R +LS Y+ + S C+R+ DC +G C C H C EG +C
 Sbjct: 171 RTTLSSKMYHTKGQEGSVCLRSSDCASGLC-----CARHFWSKICKPVLKEGQVCTKHR 224

Query: 76 FFGQ-----YRACPLRLNLTCIYSKN 96
 G ++ C C L+C K+
 Sbjct: 225 RKGSHGLEIFQRCYCGEGLSCRIQKD 250

>PIR:S37650|S37650|high-sulfur keratin - human

>STR:Q07627|Q07627|KERATIN, HIGH-SULFUR MATRIX PROTEIN,
 B2A. >GNP:X63337|X63337_1|H.sapiens HB2A gene for high
 sulfur keratin.
 Length = 177

Score = 27.8 bits (60), Expect = 7.1
 Identities = 15/36 (41%), Positives = 18/36 (49%), Gaps = 6/36 (16%)

Query: 38 SCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQT 73
 SC + CET CQ P CE+ C + S CQT
 Sbjct: 23 SCCQPSCCETSSCQ--PRCCETSCCQP----SCCQT 52

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
 Posted date: Oct 5, 2000 10:09 AM
 Number of letters in database: 24,820,038
 Number of sequences in database: 113,759

Lambda K H
 0.330 0.142 0.474

Gapped
 Lambda K H
 0.270 0.0470 0.230

blast result

GSP:W73018|W73018|Human cy)line-rich secreted protein CRSP-3.) 28 7.1
 PIR:S37650|S37650|high-sulfur keratin - human >STR:Q07627|Q0762... 28 7.1

>GSP:Y35930|Y35930|Extended human secreted protein sequence, SEQ ID
 NO. 179.
 Length = 121

Score = 263 bits (666), Expect = 6e-71
 Identities = 121/121 (100%), Positives = 121/121 (100%)

Query: 1 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH 60
 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH
 Sbjct: 1 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH 60

Query: 61 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKKMF 120
 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKKMF
 Sbjct: 61 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKKMF 120

Query: 121 F 121

F

Sbjct: 121 F 121

>GSP:Y91513|Y91513|Human secreted protein sequence encoded by gene
 63 SEQ ID NO:186.
 Length = 122

Score = 263 bits (666), Expect = 6e-71
 Identities = 121/121 (100%), Positives = 121/121 (100%)

Query: 1 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH 60
 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH
 Sbjct: 1 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH 60

Query: 61 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKKMF 120
 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKKMF
 Sbjct: 61 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKKMF 120

Query: 121 F 121

F

Sbjct: 121 F 121

>GSP:Y12687|Y12687|Human 5' EST secreted protein SEQ ID NO:277.
 Length = 120

Score = 245 bits (619), Expect = 2e-65
 Identities = 113/118 (95%), Positives = 114/118 (95%)

Query: 1 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE SCIRNQDCETGCCQ RAPDNCESH 60
 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE NQDCETGCCQ RAPDNCESH
 Sbjct: 1 MMLPQWLLLLLFLFFFLFLLTRGSLSP TKYNLLELKE XXXGNQDCETGCCQ RAPDNCESH 60

Query: 61 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLAKK 118
 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLA+K
 Sbjct: 61 CAEKGSEGLCQTQVFFGQYRACPLRNLT CIYSKNEKWL SIAYGRCQKIGRQKLARK 118

>SP:P04118|COL_HUMAN|COLIPASE PRECURSOR. >PIR:A42568 A33949
 A03163|XLHU|colipase precursor - human
 >GNP:M95529|M95529_1|Homo sapiens colipase (CLPS) gene,
 complete cds. >GNP:J02883|J02883_1|Human colipase mRNA,
 complete cds; colipase precursor.
 Length = 112

Score = 55.4 bits (131), Expect = 3e-08
 Identities = 28/84 (33%), Positives = 38/84 (44%), Gaps = 2/84 (2%)

Query: 33 LELKESCIRNQDCETGCCQ RAPDNCESHCAEKGSEGLCQTQVFFGQYRACPLRNLT CI 92
 LE E C+ + C++ CCQ + + C SE S C + +G Y CPC R LTC
 Sbjct: 28 LENGELCMNSAQCKSNCCQHSSALGLARCTSMASENSECSVKTYGIYKPCERGLTCE 87

Query: 93 YSKN--EKWLSIAYGRCQKIGRQK 114
 K + +G C GR K

Sbjct: 88 GDKTIVGSITNTNFGICHDAGRSK 111

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>PIR:S37649|S37649|high-su keratin - human
 >STR:Q07628|Q07628|KERATIN.
 >GNP:X63338|X63338_1|H.sapiens HB2B gene for high
 sulfur keratin.
 Length = 175

Score = 32.5 bits (72), Expect = 0.28
 Identities = 16/36 (44%), Positives = 19/36 (52%), Gaps = 6/36 (16%)

Query: 38 SCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQT 73
 SC + CET CCQ P CE+ C + S CQT
 Sbjct: 23 SCCQPSCCETSCCQ--PSCCETSCCQP---SCCQT 52

Score = 29.0 bits (63), Expect = 3.2
 Identities = 13/34 (38%), Positives = 19/34 (55%), Gaps = 2/34 (5%)

Query: 32 LLELKESCIRNQDCETGCCQRAPDNCESHCAEKG 65
 L++L+ SC + CET CCQ P C++ G
 Sbjct: 62 LVDLQLSCCQPSCCETSCCQ--PSCCQTSSCGTG 93

>GSP:Y44934|Y44934|Human dickkopf-1 homolog 3 protein.
 Length = 271

Score = 32.1 bits (71), Expect = 0.36
 Identities = 24/83 (28%), Positives = 34/83 (40%), Gaps = 17/83 (20%)

Query: 39 CIRNQDCETGCCQRAPDNCESH-----CAEKGSEGLCQTQVFFGQ-----YRACPLRN 88
 C+R+ DC G C C H C +G+C Q G ++ C C +
 Sbjct: 195 CLRSSDCAAGLC-----CARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKG 248

Query: 89 LTCIYSKNEKWLISIA-YGRCQKI 110
 L+C K+ + S A CQKI
 Sbjct: 249 LSCKVWKDATYSSKARLHVCQKI 271

>STR:Q9UIU3|Q9UIU3|DICKKOPF-2 PROTEIN (FRAGMENT).
 >GNP:AB035181|AB035181_1|Homo sapiens Dickkopf-2 gene,
 exon and partial cds.
 Length = 185

Score = 30.9 bits (68), Expect = 0.82
 Identities = 24/85 (28%), Positives = 35/85 (40%), Gaps = 17/85 (20%)

Query: 37 ESCIRNQDCETGCCQRAPDNCESH-----CAEKGSEGLCQTQVFFGQ-----YRACPL 86
 + C+R+ DC G C C H C +G+C Q G ++ C C
 Sbjct: 107 DPCLRSSDCIEGFC-----CARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCA 160

Query: 87 RNLTCIYSKNEKWLISIA-YGRCQKI 110
 + L+C K+ + S A CQKI
 Sbjct: 161 KGLSCKVWKDATYSSKARLHVCQKI 185

>GSP:W73019|W73019|Human cysteine-rich secreted protein CRSP-4.
 Length = 179

Score = 30.9 bits (68), Expect = 0.82
 Identities = 24/85 (28%), Positives = 35/85 (40%), Gaps = 17/85 (20%)

Query: 37 ESCIRNQDCETGCCQRAPDNCESH-----CAEKGSEGLCQTQVFFGQ-----YRACPL 86
 + C+R+ DC G C C H C +G+C Q G ++ C C
 Sbjct: 101 DPCLRSSDCIEGFC-----CARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCA 154

Query: 87 RNLTCIYSKNEKWLISIA-YGRCQKI 110
 + L+C K+ + S A CQKI
 Sbjct: 155 KGLSCKVWKDATYSSKARLHVCQKI 179

>GSP:Y99360|Y99360|Human PRO1316 (UNQ682) amino acid sequence SEQ ID
 NO:70. >GSP:Y92073|Y92073|Human DKR-2.
 >STR:Q9UBU2|Q9UBU2|DICKKOPF-2.
 >GNP:AB033208|AB033208_1|Homo sapiens dickkopf-2 mRNA,
 complete cds; 95% homologous to mouse Dkk-2 (Monaghan et

Length = 259

Score = 30.9 bits (68), Expect = 0.82
Identities = 24/85 (28%), Positives = 35/85 (40%), Gaps = 17/85 (20%)

Query: 37 ESCIRNQDCETGCCQAPDNCESH-----CAEKGSEGLCQTQVFFGQ-----YRACPCL 86
+ C+R+ DC G C C H C +G +C Q G ++ C C
Sbjct: 181 DPCLRSSDCIEGFC-----CARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCA 234
Query: 87 RNLTCTIYSKNEKWLISIA-YGRCQKI 110
+ L+C K+ + S A CQKI
Sbjct: 235 KGLSCKVWKDATYSSKARLHVCQKI 259

>GSP:Y92074|Y92074|Human DKR-2 splice variant, DKR-2a.
Length = 207

Score = 30.9 bits (68), Expect = 0.82
Identities = 24/85 (28%), Positives = 35/85 (40%), Gaps = 17/85 (20%)

Query: 37 ESCIRNQDCETGCCQAPDNCESH-----CAEKGSEGLCQTQVFFGQ-----YRACPCL 86
+ C+R+ DC G C C H C +G +C Q G ++ C C
Sbjct: 129 DPCLRSSDCIEGFC-----CARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCA 182
Query: 87 RNLTCTIYSKNEKWLISIA-YGRCQKI 110
+ L+C K+ + S A CQKI
Sbjct: 183 KGLSCKVWKDATYSSKARLHVCQKI 207

>STR:Q9Y6P9|Q9Y6P9|HJAG2.DEL-E6. >GNP:AF029779|AF029779_1|Homo
sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced
isoform of Jagged2, complete cds; An
alternatively-spliced isoform of Jagged2 with the EGF
repeat 6 deleted.
Length = 1200

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLELKECIRNQDCETGCCQAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNLT 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 343 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 399
Query: 91 CI 92
C+
Sbjct: 400 CV 401

>STR:Q9Y219|Q9Y219|JAGGED 2. >GNP:AF020201|AF020201_1|Homo sapiens
Jagged 2 mRNA, complete cds.
Length = 1238

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLELKECIRNQDCETGCCQAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNLT 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 343 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 399
Query: 91 CI 92
C+
Sbjct: 400 CV 401

>STR:Q9UNK8|Q9UNK8|JAGGED2. >GNP:AF111170|AF111170_2|Homo sapiens
14q32 Jagged2 gene, complete cds; and unknown gene;
Intron-exon boundaries were defined in relation to
Jagged2 mRNA sequence found in AF029778.
Length = 1238

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLELKECIRNQDCETGCCQAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNLT 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 343 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 399

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Query: 91 CI 92
C+
Sbjct: 400 CV 401

>STR:Q9Y6Q0|Q9Y6Q0|JAGGED2. >GNP:AF029778|AF029778_1|Homo sapiens
Jagged2 (JAG2) mRNA, complete cds; Notch ligand.
Length = 1238

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLLELKESCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNL 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 343 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 399

Query: 91 CI 92
C+
Sbjct: 400 CV 401

>STR:Q9UE99|Q9UE99|JAGGED 2. >GNP:AF003521|AF003521_1|Homo sapiens
Jagged 2 mRNA, complete cds; ligand for Notch receptor;
Contains EGF repeats and DSL domain.
Length = 1238

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLLELKESCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNL 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 343 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 399

Query: 91 CI 92
C+
Sbjct: 400 CV 401

>GSP:W05834|W05834|Human Serrate-2 (HJ2). >GSP:Y59598|Y59598|Human
Serrate protein sequence..
Length = 1257

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLLELKESCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNL 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 173 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 229

Query: 91 CI 92
C+
Sbjct: 230 CV 231

>GSP:W44298|W44298|Human serrate 2 protein fragment.
Length = 1055

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLLELKESCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNL 90
N + + +C N G C P E HC G G C + + + PC T
Sbjct: 317 NCEKAEHACTSNPCANGGSCHEVPSGFEC HC-PSGWSGPTCALDI--DECASNPCAAGGT 373

Query: 91 CI 92
C+
Sbjct: 374 CV 375

>GSP:W44299|W44299|Human serrate 2.
Length = 1212

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 NLLELKESCIRNQDCETGCCQRAPDNCESHCAEKGSEGLCQTQVFFGQYRACPCLRNL 90

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Sbjct: 317 NCEKAEHACTSNPCA)SCHEVPSGFECHEC-PSGWSGPTCALDI--DECAS)AAGGT 373

Query: 91 CI 92
C+

Sbjct: 374 CV 375

>GSP:W87895|W87895|Human JAGGED2 protein.
Length = 1148

Score = 29.7 bits (65), Expect = 1.8
Identities = 16/62 (25%), Positives = 23/62 (36%), Gaps = 3/62 (4%)

Query: 31 N L L E L K E S C I R N Q D C E T G C C Q R A P D N C E S H C A E K G S E G S L C Q T Q V F F G Q Y R A C P C L R N L T 90
N + + + C N G C P E H C G G C + + + P C T
Sbjct: 293 N C E K A E H A C T S N P C A N G G S C H E V P S G F E C H C - P S G W S G P T C A L D I - - D E C A S N P C A A G G T 349

Query: 91 CI 92
C+

Sbjct: 350 CV 351

>STR:Q9UQ12|Q9UQ12|KIAA0868 PROTEIN (FRAGMENT).
>GNP:AB020675|AB020675_1|Homo sapiens mRNA for KIAA0868
protein, partial cds.
Length = 1339

Score = 29.3 bits (64), Expect = 2.4
Identities = 12/54 (22%), Positives = 24/54 (44%)

Query: 23 G S L S P T K Y N L L E L K E S C I R N Q D C E T G C C Q R A P D N C E S H C A E K G S E G S L C Q T Q V F 76
G S + + + + C + N G C + D + + C E G G + C + +
Sbjct: 550 G S F A N V S I D M C A I I D R C V P N H C E H G G K C S Q T W D S F K C T C D E T G Y S G A T C H N S I Y 603

>STR:Q9UHC6|Q9UHC6|CELL RECOGNITION MOLECULE CASPR2.
>GNP:AF193613|AF193613_1|Homo sapiens cell recognition
molecule Caspr2 (CASPR2) mRNA, complete cds; neurexin
IV; new member of the NCP group of the Neurexin
superfamily; similar to contactin associated protein
(Caspr); Drosophila melanogaster Neurexin IV ortholog.
Length = 1331

Score = 29.3 bits (64), Expect = 2.4
Identities = 12/54 (22%), Positives = 24/54 (44%)

Query: 23 G S L S P T K Y N L L E L K E S C I R N Q D C E T G C C Q R A P D N C E S H C A E K G S E G S L C Q T Q V F 76
G S + + + + C + N G C + D + + C E G G + C + +
Sbjct: 542 G S F A N V S I D M C A I I D R C V P N H C E H G G K C S Q T W D S F K C T C D E T G Y S G A T C H N S I Y 595

>STR:Q9UE17|Q9UE17|JAGGED2 PROTEIN (FRAGMENT).
>GNP:Y14330|Y14330_1|Homo sapiens partial mRNA for
jagged2 protein.
Length = 1223

Score = 28.6 bits (62), Expect = 4.1
Identities = 16/62 (25%), Positives = 22/62 (34%), Gaps = 2/62 (3%)

Query: 31 N L L E L K E S C I R N Q D C E T G C C Q R A P D N C E S H C A E K G S E G S L C Q T Q V F F G Q Y R A C P C L R N L T 90
N + + + C N G C P E H C G G C + + + P C T
Sbjct: 327 N C E K A E H A C T S N P C A N G G S C H E V P S G F E C H C - P S G W S G P T C - A S A D I D E C A S N P C A A G G T 384

Query: 91 CI 92
C+

Sbjct: 385 CV 386

>GSP:Y04262|Y04262|Human vascular smooth muscle cell growth factor.
Length = 807

Score = 28.2 bits (61), Expect = 5.4
Identities = 21/103 (20%), Positives = 39/103 (37%), Gaps = 18/103 (17%)

Query: 34 E L K E S C I R N Q D C E T G C C Q R A P - - - - D N C E S H C A E - - - - - K G S E G S L C Q T Q V F F G 78
E E C N + + C C D C + C + + G S C
Sbjct: 543 E E M E Y C T A I I D R C V P N H C E H G G K C S Q T W D S F K C T C D E T G Y S G A T C H N S I Y 595

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